Appl. No. 09/230,195
Amdt. dated April 16, 2004
Amendment under 37 CFR 1.116 Expedited Procedure
Examining Group 1633

PATENT

Amendments to the Specification

Please replace the paragraph beginning at page 7, line 32, with the following:

--Figure 4 shows sequence details of pBAR-EDN (SEQ ID NOS:1-3).--

Please replace the paragraph beginning at page 23, line 21, with the following:

--Modified forms of ONCONASE®, including humanized ONCONASE®, and recombinant ONCONASE® (rOnc) with a variety of activating modifications are described in copending U.S. Provisional Patent Application USSN 60/011,800 filed February 21, 1996 by Rybak *et al.* Preferred rOnc molecules have an amino terminal end selected from the group consisting of: Met-Ala; Met-Arg; Met-(J); Met-Lys-(J); Met-Arg-(J); Met-Lys; Met-Lys-Pro; ~~Met-Lys-(J)-pro~~ Met-Lys-(J)-Pro (SEQ ID NO:4); Met-Lys-Pro-(J) (SEQ ID NO:5); Met-Asn; Met-Gln; Met-Asn-(J); Met-Gln-(J); Met-Asn-(J)-Pro (SEQ ID NO:6); Met-(J)-Lys; Met-(J)-Lys-Pro (SEQ ID NO:7) and Met-(J)-Pro-Lys (SEQ ID NO:8); where (J) is Ser, Tyr or Thr. In alternative forms of the rOnc molecules, the molecules employ an amino terminal end encoded by a sequence derived from the amino terminal end of EDN followed by a sequence from rOnc. In such forms, it is preferred that the amino acid sequence is one selected from the group consisting of those sequences substantially identical to those of a formula:
$Met(-1)EDN_{(1-m)}Onc_{(n-104)}$; wherein Met(-1) refers to an amino terminal residue of Met; wherein $EDN_{(1-m)}$ refers to a contiguous sequence of amino acids of a length beginning at amino acid position 1 of EDN and continuing to and including amino acid position "m" of EDN; wherein $Onc_{(n-104)}$ refers to a sequence of contiguous amino acids beginning at amino acid position "n" and continuing to and including amino acid position 104 such that: when m is 21, n is 16 or 17; when m is 22, n is 17; when m is 20, n is 16; when m is 19, n is 15; when m is 18, n is 14; when m is 17, n is 12 or 13; when m is 16, n is 11, 12, 13 or 14; when m is 15, n is 10; when m is 14, n is 9; when m is 13, n is 8; and when m is 5, n is 1. *See,* USSN 60/011,800.--

Please replace the paragraph beginning at page 40, line 11, with the following:

--SU3: 5'-AAAAGGCCT**CCCGGG**ACTGGAAGGGCTAATTCACT-3' (SEQ ID NO:9). The bases corresponding to nt. 16-35 in the LW/C viral sequence are underlined; the SmaI site is bold; sense orientation.

EU5AS: 5'-CC**GGAATTC**ACCAGTCGCCGCCCCTCGCC-3' (SEQ ID NO:10). The bases corresponding to nt. 744-763 in the LW/C viral sequence are underlined; the EcoRI site is bold; antisense orientation.

EU5S: 5'-CC**GGAATTC**GCCAAAAAATTTTGACTAGCG-3' (SEQ ID NO:11). The bases corresponding to nt. 770-790 in the LW/C viral sequence are underlined; the EcoRI site is bold; sense orientation.

XDGAS: 5[[1]]'-GGA**TCTAGATCTAGA**TTGCCCCCCTATCATTATTGT-3' (SEQ ID NO:12). The bases corresponding to nt. 2284-2305 in the HXB2 viral sequence are underlined; the XbaI sites are bold; the stop codons are double underlined; antisense orientation.

SRRES: 5'-GGACGC**GTCGAC**ACCATTAGGAGTAGCACCCAC-3' (SEQ ID NO:13). The bases corresponding to nt. 7698-7717 in the HXB2 viral sequence are underlined; the SalI site is bold; sense orientation.

BLU5AS: 5'-CGC**GGATCC**ACTGACTAAAAGGGTCTGAG-3' (SEQ ID NO:14). The bases corresponding to nt. 9681-9700 in the HXB2 viral sequence are underlined; the BamHI site is bold; antisense orientation.

ENVA: 5[[1]]'-AGAAATATCAGCACTTGTGGAGA-3' (SEQ ID NO:15). The sequence ~~correspond~~ corresponds to nt. 6237-6259 in the HXB2 viral sequence; sense orientation.

ENVB: 5[[1]]'-TGAGTGGCCCAAACATTATGTACCT-3' (SEQ ID NO:16). The sequence ~~correspond~~ corresponds to nt. 6414-6438 in the HXB2 viral sequence; antisense orientation.

ENVC: 5'-CACCACTCTATTTTGTGCATCAGATG-3' (SEQ ID NO:17). The sequence ~~correspond~~ corresponds to nt. 6369-6395 in the HXB2 viral sequence; sense orientation.

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IRESA: 5'-GC**TCTAGAG**GAATTCCGCCCCTC-3' (SEQ ID NO:18). The XbaI site is bold; the EcoRI site is underlined; sense orientation (5' of the sequence).

IRESB: [[3]]5'-GA**CTAGT**GGCAAGCTTATCATCGTG-3' (SEQ ID NO:19)[[;]]. The SpeI site is bold; antisense orientation (3' of the sequence).

EDNα: 5'-CGCGGATCCTTGATATGCTGAGTTTCGAACCA-3' (SEQ ID NO:20). Sense orientation.

EDNω: 5'-AAGGAAAAAAGCGGCCGCCTACTAGATGATACGGTCCAGA-3' (SEQ ID NO:21). Antisense orientation.

ECOSPL: 5'-GGGCGGCGACTGGTGAATT-3' (SEQ ID NO:22). Corresponding to nt. 750-768 in the pLW/C sequence. The nucleotides in bold correspond to the mutated nucleotides, with respect to pLW/C, present in pBAR and pBAR-EDN plasmids after the introduction of the ~~ECORI~~ EcoRI site. Sense orientation.

OTESAPL: 5'-TCTAACACTTCTCTCTCCGGGT-3' (SEQ ID NO:23). Corresponding to nt. 9317-9339 in the pHXB2 sequence. Antisense orientation. ~~oligonucleotides~~ Oligonucleotides 516, 477, 569F, βGS and βGAS have been described (Cara, *et al., Virology*, **208**, 242-248 (1995)).--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 11, at the end of the application.

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Amendments to the Drawings

Please replace the seven sheets of drawings with the accompanying eight replacement sheets of drawings. (Figure 2 is now two sheets instead of one.) The replacement drawings add no new matter and merely correct informalities in the drawings as originally submitted.